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 PATENT APPLICATION: US/09/771,956 DATE: 02/09/2001
 TIME: 09:35:35

Input Set : A:\Npychim1.app
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3 <110> APPLICANT: Bennett, Michele
 4 Brodbeck, Robbin
 5 Krause, James
 7 <120> TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
 9 <130> FILE REFERENCE: N2000.001
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/771,956
 C--> 12 <141> CURRENT FILING DATE: 2001-01-29
 14 <160> NUMBER OF SEQ ID NOS: 31
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1605
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
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 26 ctgaacagt gacctgtttt gaaagaaacat actgtccatt tgcataaaat aatctataac 180
 27 uaccaaaccat atcaaaatgtt attcaacattt atttttccag gtgaaaatc attcagtccaa 240
 28 ctctaatttc tcagagaaga atgcccacgt tctggctttt gaaaatgtatg attgtcatct 300
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 30 ctctggaaac ctggccttga tcataatcat ctgtggaaacaa aaggagatgt gaaatgttac 420
 31 caacatcctg attgtgaacc ttcccttcctc agacttgctt gtgtccatca tttgtctccc 480
 32 ctttacattt gtctacatcat taatggacca ctgggtctttt ggtgaggcgtt tttgttaatgtt 540
 33 gaatccctttt gtgcaatgtt tttcaatcac tttttttttt tttttttttt tttttttttt 600
 34 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 660
 35 ttatgttaggtt attgtgttga ttggggctt tttttttttt tttttttttt tttttttttt 720
 36 ctaccaatgtt atgactgttgc agccgttccaa aaatgttacaa ctgtatgttgcgtt acaaagacaa 780
 37 atacgtgttgc ttttgcattt tttccatggaa ctctccatggaa tttttttttt tttttttttt 840
 38 ctgggtctt cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 900
 39 tatacgcctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 960
 40 cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1020
 41 ctggccttccatcttaccatctt tttttttttt tttttttttt tttttttttt tttttttttt 1080
 42 ctggccttccatcttaccatctt tttttttttt tttttttttt tttttttttt tttttttttt 1140
 43 caaccccaat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1200
 44 caactttttt gatttccgtt ctgggatgtt tttttttttt tttttttttt tttttttttt 1260
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 55 <212> TYPE: PRT
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 58 <400> SEQUENCE: 2
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63          20          25          30
65 Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
66          35          40          45
68 Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
69          50          55          60
71 Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val
72 65          70          75          80
74 Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe
75          85          90          95
77 Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
78          100         105         110
80 Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
81          115         120         125
83 Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
84          130         135         140
86 Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala
87 145         150         155         160
89 Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr
90          165         170         175
92 Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
93          180         185         190
95 Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg
96          195         200         205
98 Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
99          210         215         220
101 Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
102 225         230         235         240
104 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
105          245         250         255
107 Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
108          260         265         270
110 Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
111          275         280         285
113 Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
114          290         295         300
116 Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
117 305         310         315         320
119 Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Asn
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122 Phe Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu Thr Ile Ala Met
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125 Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
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135 <210> SEQ ID NO: 3
136 <211> LENGTH: 382

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Input Set : A:\Npychim1.app
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137 <212> TYPE: PRT
138 <213> ORGANISM: Rattus norvegicus
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147 His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ala Tyr Gly Ala
148 35 40 45
150 Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
151 50 55 60
153 Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
154 65 70 75 80
156 Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
157 85 90 95
159 Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
160 100 105 110
162 Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
163 115 120 125
165 Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
166 130 135 140
168 Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
169 145 150 155 160
171 Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln
172 165 170 175
174 Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys
175 180 185 190
177 Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu
178 195 200 205
180 Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
181 210 215 220
183 Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg
184 225 230 235 240
186 Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu
187 245 250 255
189 Thr Lys Arg Ile Asn Val Met Leu Leu Ser Ile Val Val Ala Phe Ala
190 260 265 270
192 Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn
193 275 280 285
195 His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys
196 290 295 300
198 His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly
199 305 310 315 320
201 Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe
202 325 330 335
204 Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu Thr Ile Ala Met Ser
205 340 345 350
207 Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro
208 355 360 365

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Input Set : A:\Npychim1.app
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 215 <211> LENGTH: 1406
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 217 <213> ORGANISM: Homo sapiens
 219 <400> SEQUENCE: 4
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 222 tgatttccca gtctggatg actataaaaag cagtgtatg gacttacagt attttctgat 180
 223 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaatggc 240
 224 tctcatgaaa aagcgtatac agaagactac ggtaaacttc ctcataggca atctggcctt 300
 225 ttctgtatc ttgggttgc tgggttgc accttcaca ctgacgtctg tcttgctgga 360
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 227 ttgggttca actttaattt taatataatcaat tgccattgtc aggtatcata tgataaaaaca 480
 228 tcccatatct aataatttaa cagcaaacc a tggtacttt ctgatagcta ctgtctggac 540
 229 actaggttt gccatctgtt ctcccttcc agtggttcac agtcttggg aacttcaaga 600
 230 aacatttggt tcagcattgc tgagcagcag gtattatgtt gttgagtcat ggccatctga 660
 231 ttccatcaga attgcatttca ctatctttt attgttagtt cagttatc tggcccttagt 720
 232 ttgtcttact gtaagtataa caagtgtc cagaagtata aytgtggat tggccaaacaa 780
 233 agaaaacaga cttgaagaaa atgagatgt caacttaact ttcatccat ccaaaaagag 840
 234 tggccttcag gtgaaactct ctggcageca taaatggagt tatttattca tcaaaaacaa 900
 235 cagaagaaga tatagcaaga agacagcatg tgggttacct gctccagaaa gacccatctca 960
 236 agagaaccac tcccaataac ttccagaaaa ctggctctt gtaagaagtc agctctcttc 1020
 237 atccagtagt ttccatcagg ggytccccac ttgtttttagt aaaaatctg aagaaaattc 1080
 238 agatgttcat gatttggag taaaacgttc ttgttacaaga ataaaaaaaagatctcgaag 1140
 239 tgggttctac agactgacca tactgtatatt agtatttgc gtttagttgga tggccactaca 1200
 240 ccttttccat gtggtaactg attttaatga caatcttatt tcaaatagcc atttcaagg 1260
 241 ggtgtattgc atttgcattt tggggcat gatgtccctgt tggcttatac caattctata 1320
 242 tgggtttctt aataatggg ttaaagctga tttagtgc cttatataact gtcttcatat 1380
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 249 <213> ORGANISM: Artificial Sequence
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 252 <223> OTHER INFORMATION: Description of Artificial Sequence: Y5/Y1 CHIMERA
 254 <400> SEQUENCE: 5
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 257 tgatttccca gtctggatg actataaaaag cagtgtatg gacttacagt attttctgat 180
 258 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaatggc 240
 259 tctcatgaaa aagcgtatac agaagactac ggtaaacttc ctcataggca atctggcctt 300
 260 ttctgtatc ttgggttgc tgggttgc accttcaca ctgacgtctg tcttgctgga 360
 261 tcagtggatg ttggcaaaag tcatgtgcca tattatgcct ttcttcaat gtgtgtcagt 420
 262 ttgggttca actttaattt taatataatcaat tgccattgtc aggtatcata tgataaaaaca 480
 263 tcccatatct aataatttaa cagcaaacc a tggtacttt ctgatagcta ctgtctggac 540
 264 actaggttt gccatctgtt ctcccttcc agtggttcac agtcttggg aacttcaaga 600
 265 aacatttggt tcagcattgc tgagcagcag gtattatgtt gttgagtcat ggccatctga 660

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266 ttcatacaga attgcctta ctatctttt attgtctttt cagttatattc tgcccttagt 720
 267 ttgtctttact gtaagtcata caagtgtctg cattacgccta aaaaggagaa acaacatgt 780
 268 ggacaagatg agagacaata agtacaggtc cagtagatct cgaagtgttt tctacagact 840
 269 gaccatactt atttagttat ttgtcttttag ttggatgcca ctacacccctt tccatgtgg 900
 270 aactgatttt aatgacacatc ttatltcaaa taggcatttc aagtttgggtt attgcattt 960
 271 tcattttgtt ggcatgtgt cctgttgtct taatccaatt ctatatgggt ttcttaataa 1020
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 276 <211> LENGTH: 350
 277 <212> TYPE: PRT
 278 <213> ORGANISM: Artificial Sequence
 280 <220> FEATURE:
 281 <223> OTHER INFORMATION: Description of Artificial Sequence: Y5/Y1 CHIMERA
 283 <400> SEQUENCE: 6
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 287 Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr
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 290 Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
 291 35 40 45
 293 Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
 294 50 55 60
 296 Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
 297 65 70 75 80
 299 Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
 300 85 90 95
 302 Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
 303 100 105 110
 305 Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
 306 115 120 125
 308 Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
 309 130 135 140
 311 Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
 312 145 150 155 160
 314 Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
 315 165 170 175
 317 Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
 318 180 185 190
 320 Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys
 321 195 200 205
 323 Val. Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser
 324 210 215 220
 326 Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser
 327 225 230 235 240
 329 His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met Asp
 330 245 250 255
 332 Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val Phe
 333 260 265 270
 335 Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro

VERIFICATION SUMMARY
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date